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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=1; day=29; hr=12; min=49; sec=53; ms=72;]

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Application No: 10516558

Version No: 3.0

Input Set:

Output Set:

Started: 2008-01-16 18:19:50.998

Finished: 2008-01-16 18:19:54.578

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 580 ms

Total Warnings: 182

Total Errors: 0

No. of SeqIDs Defined: 182

Actual SeqID Count: 182

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-01-16 18:19:50.998
Finished: 2008-01-16 18:19:54.578
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 580 ms
Total Warnings: 182
Total Errors: 0
No. of SeqIDs Defined: 182
Actual SeqID Count: 182

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (133)
W 402	Undefined organism found in <213> in SEQ ID (134)
W 402	Undefined organism found in <213> in SEQ ID (135)
W 402	Undefined organism found in <213> in SEQ ID (136)
W 402	Undefined organism found in <213> in SEQ ID (137)
W 402	Undefined organism found in <213> in SEQ ID (138)
W 402	Undefined organism found in <213> in SEQ ID (139)
W 402	Undefined organism found in <213> in SEQ ID (140)
W 402	Undefined organism found in <213> in SEQ ID (141)
W 402	Undefined organism found in <213> in SEQ ID (142)
W 402	Undefined organism found in <213> in SEQ ID (143)
W 402	Undefined organism found in <213> in SEQ ID (144)
W 402	Undefined organism found in <213> in SEQ ID (145)
W 402	Undefined organism found in <213> in SEQ ID (146)
W 402	Undefined organism found in <213> in SEQ ID (147)
W 402	Undefined organism found in <213> in SEQ ID (148)
W 402	Undefined organism found in <213> in SEQ ID (149)
W 402	Undefined organism found in <213> in SEQ ID (150)
W 402	Undefined organism found in <213> in SEQ ID (151)
W 402	Undefined organism found in <213> in SEQ ID (152)
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Chano, Tokuhiko
Okabe, Hidetoshi
Ikegawa, Shiro

<120> RB1 gene induced protein (RB1CC1) and gene

<130> 3190-070

<140> 10516558

<141> 2005-01-25

<150> PCT/JP03/00882

<151> 2003-01-30

<150> JP P2002-161400

<151> 2002-06-03

<150> JP P2002-214978

<151> 2002-07-24

<160> 182

<170> PatentIn version 3.5

<210> 1

<211> 1594

<212> PRT

<213> Unknown

<220>

<223> human RB1CC1

<400> 1

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20 25 30

Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
35 40 45

Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
50 55 60

Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
65 70 75 80

Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
85 90 95

Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
100 105 110

His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
115 120 125

Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
130 135 140

Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
145 150 155 160

Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
165 170 175

Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
180 185 190

Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
195 200 205

Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
210 215 220

Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
225 230 235 240

Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
245 250 255

Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala
260 265 270

Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
275 280 285

Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
290 300

Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp

305		310		315		320
Val Glu Ser Leu	Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp					
	325		330		335	
Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala						
	340		345		350	
Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg						
	355		360		365	
Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn						
	370		375		380	
Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala						
385		390		395		400
Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His						
	405		410		415	
Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp						
	420		425		430	
Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu						
	435		440		445	
His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln						
	450		455		460	
Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu						
465		470		475		480
Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr						
	485		490		495	
Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His						
	500		505		510	
Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr						
	515		520		525	
Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys						
	530		535		540	

Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro
545 550 555 560

Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
565 570 575

Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
580 585 590

Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
595 600 605

His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
610 615 620

Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
625 630 635 640

Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
645 650 655

Glu Ser Thr Ala Gly Ile Thr Thr Thr Thr Ser Pro Arg Thr Pro Pro
660 665 670

Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
675 680 685

Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
690 695 700

Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
705 710 715 720

Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
725 730 735

Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
740 745 750

Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
755 760 765

Ile	Asn	Ala	Ile	Asp	Ser	Arg	Arg	Met	Gln	Asp	Thr	Asn	Val	Cys	Gly	770	775	780
Lys	Glu	Asp	Phe	Gly	Asp	His	Thr	Ser	Leu	Asn	Val	Gln	Leu	Glu	Arg	785	790	795 800
Cys	Arg	Val	Val	Ala	Gln	Asp	Ser	His	Phe	Ser	Ile	Gln	Thr	Ile	Lys	805	810	815
Glu	Asp	Leu	Cys	His	Phe	Arg	Thr	Phe	Val	Gln	Lys	Glu	Gln	Cys	Asp	820	825	830
Phe	Ser	Asn	Ser	Leu	Lys	Cys	Thr	Ala	Val	Glu	Ile	Arg	Asn	Ile	Ile	835	840	845
Glu	Lys	Val	Lys	Cys	Ser	Leu	Glu	Ile	Thr	Leu	Lys	Glu	Lys	His	Gln	850	855	860
Lys	Glu	Leu	Leu	Ser	Leu	Lys	Asn	Glu	Tyr	Glu	Gly	Lys	Leu	Asp	Gly	865	870	875 880
Leu	Ile	Lys	Glu	Thr	Glu	Glu	Asn	Glu	Asn	Lys	Ile	Lys	Lys	Leu	Lys	885	890	895
Gly	Glu	Leu	Val	Cys	Leu	Glu	Glu	Val	Leu	Gln	Asn	Lys	Asp	Asn	Glu	900	905	910
Phe	Ala	Leu	Val	Lys	His	Glu	Lys	Glu	Ala	Val	Ile	Cys	Leu	Gln	Asn	915	920	925
Glu	Lys	Asp	Gln	Lys	Leu	Leu	Glu	Met	Glu	Asn	Ile	Met	His	Ser	Gln	930	935	940
Asn	Cys	Glu	Ile	Lys	Glu	Leu	Lys	Gln	Ser	Arg	Glu	Ile	Val	Leu	Glu	945	950	955 960
Asp	Leu	Lys	Lys	Leu	His	Val	Glu	Asn	Asp	Glu	Lys	Leu	Gln	Leu	Leu	965	970	975
Arg	Ala	Glu	Leu	Gln	Ser	Leu	Glu	Gln	Ser	His	Leu	Lys	Glu	Leu	Glu	980	985	990

Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr
995 1000 1005

Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln
1010 1015 1020

Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu
1025 1030 1035

Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu
1040 1045 1050

Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu
1055 1060 1065

Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala
1070 1075 1080

Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu
1085 1090 1095

Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp
1100 1105 1110

Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu
1115 1120 1125

Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg
1130 1135 1140

His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val
1145 1150 1155

Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys
1160 1165 1170

Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser
1175 1180 1185

Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu
1190 1195 1200

Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys

1205	1210	1215
Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys		
1220	1225	1230
Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu		
1235	1240	1245
Phe Lys Leu Glu Arg Glu Val Val Glu Lys Glu Leu Leu Glu Lys		
1250	1255	1260
Val Lys His Leu Glu Asn Gln Ile Ala Lys Ser Pro Ala Ile Asp		
1265	1270	1275
Ser Thr Arg Gly Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu		
1280	1285	1290
Lys Leu Gln Glu Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu		
1295	1300	1305
Gln Glu Lys Arg Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser		
1310	1315	1320
Leu Ile Ala Glu Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg		
1325	1330	1335
Glu Lys Met Arg Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys		
1340	1345	1350
Leu Lys Ser Thr Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile		
1355	1360	1365
Glu Ser Leu Ser Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys		
1370	1375	1380
Lys Leu Glu Glu Glu Val Ser Lys Leu Arg Ser Ser Ser Phe Val		
1385	1390	1395
Pro Ser Pro Tyr Val Ala Thr Ala Pro Glu Leu Tyr Gly Ala Cys		
1400	1405	1410
Ala Pro Glu Leu Pro Gly Glu Ser Asp Arg Ser Ala Val Glu Thr		
1415	1420	1425

Ala Asp Glu Gly Arg Val Asp Ser Ala Met Glu Thr Ser Met Met
1430 1435 1440

Ser Val Gln Glu Asn Ile His Met Leu Ser Glu Glu Lys Gln Arg
1445 1450 1455

Ile Met Leu Leu Glu Arg Thr Leu Gln Leu Lys Glu Glu Glu Asn
1460 1465 1470

Lys Arg Leu Asn Gln Arg Leu Met Ser Gln Ser Met Ser Ser Val
1475 1480 1485

Ser Ser Arg His Ser Glu Lys Ile Ala Ile Arg Asp Phe Gln Val
1490 1495 1500

Gly Asp Leu Val Leu Ile Ile Leu Asp Glu Arg His Asp Asn Tyr
1505 1510 1515

Val Leu Phe Thr Val Ser Pro Thr Leu Tyr Phe Leu His Ser Glu
1520 1525 1530

Ser Leu Pro Ala Leu Asp Leu Lys Pro Gly Glu Gly Ala Ser Gly
1535 1540 1545

Ala Ser Arg Arg Pro Trp Val Leu Gly Lys Val Met Glu Lys Glu
1550 1555 1560

Tyr Cys Gln Ala Lys Lys Ala Gln Asn Arg Phe Lys Val Pro Leu
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Gly Thr Lys Phe Tyr Arg Val Lys Ala Val Ser Trp Asn Lys Lys
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20 25 30

Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
35 40 45

Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
50 55 60

Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
65 70 75 80

Cys Asp Arg Ala Pro Ala Ile Pro Lys Ala Thr Phe Ser Thr Glu Asn
85 90 95

Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
100 105 110

His Thr Val Ala Ser Arg Thr Gln Leu Ala Val Glu Met Tyr Asp Val
115 120 125

Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
130 135 140

Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
145 150 155 160

Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
165 170 175

Asp Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
180 185 190

Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
195 200 205

Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Pro Asp Ser Leu Asn
210 215 220

Glu His Glu Gly Ser Glu Lys Ala Glu Met Lys Arg Ser Thr Glu Leu
225 230 235 240

Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Thr Ser Leu Val Thr
245 250 255

Ser Phe His Lys Ser Met Glu His Val Ala Pro Asp Pro Thr Gly Thr
260 265 270

Glu Arg Gly Lys Glu Leu Arg Glu Ser Cys Gln Ser Thr Val Gln Gln
275 280 285

Glu Glu Ala Ser Val Asp Ala Lys Asp Ser Asp Leu Pro Phe Phe Asn
290 295 300

Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp Val
305 310 315 320

Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp Pro
325 330 335

Lys Ile Ile Gln Pro Phe Met Leu Glu Cys His Gln Thr Ile Ala Lys
340 345 350

Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg Leu
355 360 365

Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Ser Arg Leu Val Asn Glu
370 375 380

Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Met Arg Ala Glu
385 390 395 400

Asn